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Genome Announcements

# Genome sequence of *Bradyrhizobium embrapense* strain CNPSo 2833$^T$, isolated from a root nodule of *Desmodium heterocarpon*

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ABSTRACT

*Bradyrhizobium embrapense* CNPSo 2833$^T$ is a nitrogen-fixing symbiont of the legume pasture *Desmodium*. Its draft genome contains 8,267,832 bp and 7876 CDSs. The symbiotic island includes nodulation and nitrogen fixation genes resembling the operon organization of *B. japonicum*. Several CDSs related to secretion proteins and stress tolerance were also identified.

## Genome announcement

The nitrogen-fixing symbioses of bacteria collectively called as "rhizobia" and plants of the family Leguminosae (=Fabaceae) can contribute with high amounts of nitrogen to agronomic crops, forests and pastures. Selection programs to identify elite rhizobial strains for each legume and the practice of inoculation can greatly impact agronomic and environmental sustainability, decreasing the use of chemical N fertilizers.[1,2]

The genus *Bradyrhizobium* occupies a variety of ecosystems and is enriched in living styles,[2,3] representing the most abundant rhizobial group in tropical soils.[1] In the past few years, our group has reported large genetic diversity among Brazilian *Bradyrhizobium* strains,[4–6] and has also described new *Bradyrhizobium* species.[7–9]

Here we report the draft genome of the new species *Bradyrhizobium embrapense* strain CNPSo 2833$^T$ (=CIAT 2372$^T$ = BR 2212$^T$ = SEMIA 6208$^T$ = U674$^T$), an important symbiont of the tropical legume pasture *Desmodium heterocarpon* (former *D. ovalifolium*). The strain has been successfully used in commercial inoculants for this legume in Brazil since 1988.[8]

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To access the bacterial genome sequence, total DNA was extracted using the DNeasy Blood and Tissue Kit (Qiagen) and processed on the MiSeq plataform (Illumina) at Embrapa Soja, Londrina, Brazil. Shotgun sequencing generated 646,023 paired-end reads (2× 300 bp), corresponding to approximately 21.5-fold coverage. The FASTQ files were *de novo* assembled by A5-miseq pipeline, which performs read trimming, contig assembly, misassembly correction and final scaffolding.[10]

Sequences were submitted to RAST,[11] and the genome estimated at 8,267,832 bp, with one circular chromosome assembled in 36 contigs. Annotation identified 7876 CDSs (coding DNA sequences). This number of predicted genes is lower than in *B. japonicum* and *B. diazoefficiens*.[12] The analysis at the SEED system[13] allowed the classification of 40% of the CDSs in 505 subsystems. The major categories of putative genes were of the metabolism of carbohydrates (14.4%) and amino acids and derivatives (12.9%). A symbiotic island was identified resembling that of *B. japonicum*,[12] with two copies of the regulatory *nodD* gene, the operon *nodABCSUIJ* and also *nol*YK, *nolNO* and *nodZ*; some of these genes play important roles in host specificity.[14] The island also carries the genes coding for the nitrogenase. The genome is enriched in genes of the Type I, II, III and IV secretion systems and carries 206 CDSs related to stress response.

The information obtained with genome of *B. embrapense* contributes to our still poor knowledge of the diversity of tropical rhizobia.

Nucleotide sequence accession number. The whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number SUBID (SUB985051), BioProject (PRJNA287423), BioSample (SAMN03782074), Accession (LFIP00000000). The version described in this paper is LFIP02000000.

## Conflicts of interest

The authors declare no conflicts of interest.

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